

Attorney docket 38-21(52529)B

REMARKS

The Office Action states that the application contains claims directed to patentable distinct and divergent species of the claimed invention and Applicant is required to make the following three species election for purpose of examination (i.e. Species I, Species II, and Species III):

Species I: Method as set forth in Claim 1, wherein a combination of feature variables from step a) is assessed using two of the feature variables disclosed in Table 1 to start examination.

Species II: Method as set forth in Claim 1, wherein the scoring functions from step d) is assessed using two of the scoring function disclosed in Table 2 to start examination.

Species III: Method as set forth in Claim 1, wherein the combination of feature variables from step c) is assessed using two of the scoring function disclosed in Table 3 to start examination.

Applicants respectfully traverse the species election requirement and provisionally elect the species as the followings;

Specie I : Kozak Consensus and Frame-Specific Base Composition from Table 1

Specie II: Bayes Network Score and Frame-specific Monomer Score from Table 2

Specie III: net8 (Class = Bayes network; Begin = ATG - 9; End = ATG + 5; Prior = 0.8)
and dfm2 (Class = Frame-specific monomer; Begin = ATG + 0; End = ATG + 50; prior = 0.5; frame = 2)

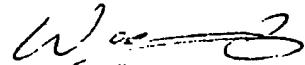
Furthermore, Applicant respectfully submits that the species identification that is simply divided by individual table or each entry in Table 1, 2, and 3, as stated in the Office Action, lacks of scientific soundness and thus is improper. Table 1 lists several nucleotide sequence characteristics that can be measured to detect the presence or

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absence of an initiator codon. This is not an exhaustive list of observable nucleotide sequence characteristics; many others appear in the scientific literature. The Applicant simply found these to be particularly useful. Table 2 lists generic scoring functions that can be used to measure the characteristics listed in Table 1. Other scoring functions exist that are not listed in Table 2, but again the functions listed are those that were found to be especially useful. Table 3 lists scoring function parameters that affect how accurately the outputs of the various scoring functions measure the sequence characteristics of Table 1, and thereby reveal the presence or absence of an initiator codon. Although many different parameter values are listed in Table 3, plainly there are an infinite number of variations that are not listed. Therefore, it is not the Applicant's intent to pre-select particular combinations of feature variables, scoring functions, and parameters. Rather, the Applicant's invention is directed to a method of detecting translation initiation codons, which involves training and applying quadratic discriminant functions to the problem of detecting initiation codons, and hereby finding optimal combinations of feature variables, scoring functions, and parameters in a specific context so that an accurate detection of translation initiation codon can be achieved. Example 1 illustrates one of the embodiments of such method.

Based upon the foregoing, Applicant submits that the species election requirement is improper and therefore should be withdrawn. If the Examiner has any question regarding this application, the Examiner is encouraged to contact Applicant's undersigned representative at 636-737-6460.

Respectfully submitted,


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Date: March 1, 2006